

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/816, 276A
Source: 1FW16
Date Processed by STIC: 3/9/07

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 03/09/2007

PATENT APPLICATION: US/10/816,276A

TIME: 11:25:18

Input Set : F:\NS\NS.txt

Output Set: N:\CRF4\03092007\J816276A.raw

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3 <110> APPLICANT: BETTER, Marc D.
4   HORWITZ, Arnold H.
6 <120> TITLE OF INVENTION: HUMAN ENGINEERED TO ANTIBODIES TO EP-CAM
8 <130> FILE REFERENCE: 117791-072
10 <140> CURRENT APPLICATION NUMBER: US 10/816,276A
11 <141> CURRENT FILING DATE: 2004-03-31
13 <150> PRIOR APPLICATION NUMBER: US 60/459,334
14 <151> PRIOR FILING DATE: 2003-03-31
16 <160> NUMBER OF SEQ ID NOS: 61
18 <170> SOFTWARE: PatentIn version 3.2
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22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
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26 <221> NAME/KEY: misc_feature
27 <223> OTHER INFORMATION: Mouse Human Chimeric Light Chain DNA and Protein
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (1)..(717)
33 <220> FEATURE:
34 <221> NAME/KEY: mat_peptide
35 <222> LOCATION: (61)..()
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40   -20                      -15                      -10                      -5
41   gga tcc act gca gat att gtg atg acg cag gct gca ttc tcc aat cca      96
42   Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ala Ala Phe Ser Asn Pro
43   -1  1                      5                      10
44   gtc act ctt gga aca tca ggt tcc atc tcc tgc agg tct agt aag agt      144
45   Val Thr Leu Gly Thr Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
46   15                      20                      25
47   ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aag      192
48   Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
49   30                      35                      40
50   cca ggc cag tct cct cag ctc ctg att tat cag atg tcc aac ctt gcc      240
51   Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala
52   45                      50                      55                      60
53   tca gga gtc cca gac agg ttc agt agc agt ggg tca gga act gat ttc      288
54   Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
55   65                      70                      75
56   aca ctg aga atc agc aga gtg gag gct gag gat gtg ggt gtt tat tac      336

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60   Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gly Gly Thr Lys
61           95           100           105
62   ctt gag atg aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg      432
63   Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
64           110           115           120
65   cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg      480
66   Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
67           125           130           135           140
68   ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat      528
69   Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
70           145           150           155
71   aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac      576
72   Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
73           160           165           170
74   agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa      624
75   Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
76           175           180           185
77   gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag      672
78   Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
79           190           195           200
80   ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag      720
81   Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
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85 <211> LENGTH: 239
86 <212> TYPE: PRT
87 <213> ORGANISM: Homo sapiens
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91   -20           -15           -10           -5
92   Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ala Ala Phe Ser Asn Pro
93           -1 1           5           10
94   Val Thr Leu Gly Thr Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
95           15           20           25
96   Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
97           30           35           40
98   Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala
99           45           50           55           60
100   Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
101           65           70           75
102   Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
103           80           85           90
104   Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gly Gly Thr Lys
105           95           100           105
106   Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
107           110           115           120

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108      Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
109      125                      130                      135                      140
110      Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
111                      145                      150                      155
112      Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
113                      160                      165                      170
114      Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
115                      175                      180                      185
116      Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
117                      190                      195                      200
118      Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
119      205                      210                      215
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122 <211> LENGTH: 1398
123 <212> TYPE: DNA
124 <213> ORGANISM: Homo sapiens
126 <220> FEATURE:
127 <221> NAME/KEY: misc_feature
128 <223> OTHER INFORMATION: Mouse-Human chimeric Heavy Chain DNA and Protein Sequence
130 <220> FEATURE:
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132 <222> LOCATION: (1)..(1395)
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141                      -15                      -10                      -5
142      gcc caa gca cag atc cag ttg gtg cag tct gga cct gag ctg aag aag      96
143      Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
144      -1 1                      5                      10
145      cct gga gag aca gtc aag atc tcc tgc aag gct tct gga tat acc ttc      144
146      Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
147      15                      20                      25
148      aca aaa tat gga atg aac tgg gtg aag cag gct cca gga aag ggt tta      192
149      Thr Lys Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu
150      30                      35                      40                      45
151      aag tgg atg ggc tgg ata aac acc tac act gaa gag cca aca tat ggt      240
152      Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Glu Glu Pro Thr Tyr Gly
153                      50                      55                      60
154      gat gac ttc aag gga cgg ttt gcc ttc tct ttg gaa acc tct gcc agc      288
155      Asp Asp Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser
156                      65                      70                      75
157      act gcc aat ttg cag atc aac aac ctc aaa agt gag gac acg gct aca      336
158      Thr Ala Asn Leu Gln Ile Asn Asn Leu Lys Ser Glu Asp Thr Ala Thr
159      80                      85                      90
160      tat ttc tgt gca aga ttt ggc tct gct gtg gac tac tgg ggt caa gga      384
161      Tyr Phe Cys Ala Arg Phe Gly Ser Ala Val Asp Tyr Trp Gly Gln Gly

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164	Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe			
165	110 115 120 125			
166	ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg	480		
167	Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu			
168	130 135 140			
169	ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tgc tgg	528		
170	Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp			
171	145 150 155			
172	aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta	576		
173	Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu			
174	160 165 170			
175	cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc	624		
176	Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser			
177	175 180 185			
178	agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc	672		
179	Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro			
180	190 195 200 205			
181	agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt gac aaa	720		
182	Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys			
183	210 215 220			
184	act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg	768		
185	Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro			
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187	tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc	816		
188	Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser			
189	240 245 250			
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191	Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp			
192	255 260 265			
193	cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat	912		
194	Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn			
195	270 275 280 285			
196	gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac cgg gtg	960		
197	Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val			
198	290 295 300			
199	gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag	1008		
200	Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu			
201	305 310 315			
202	tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa	1056		
203	Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys			
204	320 325 330			
205	acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc	1104		
206	Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr			
207	335 340 345			
208	ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc ctg acc	1152		
209	Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr			
210	350 355 360 365			

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212      Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
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214      agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg      1248
215      Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
216              385              390              395
217      gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag      1296
218      Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
219              400              405              410
220      agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag      1344
221      Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
222              415              420              425
223      gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt      1392
224      Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
225      430              435              440              445
226      aaa tga      1398
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230 <211> LENGTH: 465
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232 <213> ORGANISM: Homo sapiens
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238              -1 1              5              10
239      Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
240              15              20              25
241      Thr Lys Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu
242      30              35              40              45
243      Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Glu Glu Pro Thr Tyr Gly
244              50              55              60
245      Asp Asp Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser
246              65              70              75
247      Thr Ala Asn Leu Gln Ile Asn Asn Leu Lys Ser Glu Asp Thr Ala Thr
248              80              85              90
249      Tyr Phe Cys Ala Arg Phe Gly Ser Ala Val Asp Tyr Trp Gly Gln Gly
250              95              100              105
251      Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
252      110              115              120              125
253      Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
254              130              135              140
255      Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
256              145              150              155
257      Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
258              160              165              170
259      Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
260              175              180              185
261      Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro

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VERIFICATION SUMMARY

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